

SEQUENCE LISTING

<110> Zhou, Ming-Ming

<120> METHODS OF IDENTIFYING MODULATORS OF THE FGF RECEPTOR

<130> 2459-1-002N

<140> UNKNOWN

<141> 2001-01-11

<150> 60/175,867

<151> 2000-01-12

<160> 7

<170> PatentIn Ver. 2.0

<210> 1

<211> 508

<212> PRT

<213> Homo sapien

<400> 1

Met	Gly	Ser	Cys	Cys	Ser	Cys	Pro	Asp	Lys	Asp	Thr	Val	Pro	Asp	Asn
1				5					10					15	

His	Arg	Asn	Lys	Phe	Lys	Val	Ile	Asn	Val	Asp	Asp	Asp	Gly	Asn	Glu
		20						25					30		

Leu	Gly	Ser	Gly	Ile	Met	Glu	Leu	Thr	Asp	Thr	Glu	Leu	Ile	Leu	Tyr
		35					40					45			

Thr	Arg	Lys	Arg	Asp	Ser	Val	Lys	Trp	His	Tyr	Leu	Cys	Leu	Arg	Arg
	50					55					60				

Tyr	Gly	Tyr	Asp	Ser	Asn	Leu	Phe	Ser	Phe	Glu	Ser	Gly	Arg	Arg	Cys
65					70					75					80

Gln	Thr	Gly	Gln	Gly	Ile	Phe	Ala	Phe	Lys	Cys	Ala	Arg	Ala	Glu	Glu
			85						90					95	

Leu	Phe	Asn	Met	Leu	Gln	Glu	Ile	Met	Gln	Asn	Asn	Ser	Ile	Asn	Val
			100					105					110		

Val	Glu	Glu	Pro	Val	Val	Glu	Arg	Asn	Asn	His	Gln	Thr	Glu	Leu	Glu
			115				120					125			

Val Pro Arg Thr Pro Arg Thr Pro Thr Thr Pro Gly Phe Ala Ala Gln
 130 135 140
 Asn Leu Pro Asn Gly Tyr Pro Arg Tyr Pro Ser Phe Gly Asp Ala Ser
 145 150 155 160
 Ser His Pro Ser Ser Arg His Pro Ser Val Gly Ser Ala Arg Leu Pro
 165 170 175
 Ser Val Gly Glu Glu Ser Thr His Pro Leu Leu Val Ala Glu Glu Gln
 180 185 190
 Val His Thr Tyr Val Asn Thr Thr Gly Val Gln Glu Glu Arg Lys Asn
 195 200 205
 Arg Thr Ser Val His Val Pro Leu Glu Ala Arg Val Ser Asn Ala Glu
 210 215 220
 Ser Ser Thr Pro Lys Glu Glu Pro Ser Ser Ile Glu Asp Arg Asp Pro
 225 230 235 240
 Gln Ile Leu Leu Glu Pro Glu Gly Val Lys Phe Val Leu Gly Pro Thr
 245 250 255
 Pro Val Gln Lys Gln Leu Met Glu Lys Glu Lys Leu Glu Gln Leu Gly
 260 265 270
 Arg Asp Gln Val Ser Gly Ser Gly Ala Asn Asn Thr Glu Trp Asp Thr
 275 280 285
 Gly Tyr Asp Ser Asp Glu Arg Arg Asp Ala Pro Ser Val Asn Lys Leu
 290 295 300
 Val Tyr Glu Asn Ile Asn Gly Leu Ser Ile Pro Ser Ala Ser Gly Val
 305 310 315 320
 Arg Arg Gly Arg Leu Thr Ser Thr Ser Thr Ser Asp Thr Gln Asn Ile
 325 330 335
 Asn Asn Ser Ala Gln Arg Arg Thr Ala Leu Leu Asn Tyr Glu Asn Leu
 340 345 350
 Pro Ser Leu Pro Pro Val Trp Glu Ala Arg Lys Leu Ser Arg Asp Glu
 355 360 365
 Asp Asp Asn Leu Gly Pro Lys Thr Pro Ser Leu Asn Gly Tyr His Asn
 370 375 380

Asn Leu Asp Pro Met His Asn Tyr Val Asn Thr Glu Asn Val Thr Val
 385 390 395 400

Pro Ala Ser Ala His Lys Ile Glu Tyr Ser Arg Arg Arg Asp Cys Thr
 405 410 415

Pro Thr Val Phe Asn Phe Asp Ile Arg Arg Pro Ser Leu Glu His Arg
 420 425 430

Gln Leu Asn Tyr Ile Gln Val Asp Leu Glu Gly Gly Ser Asp Ser Asp
 435 440 445

Asn Pro Gln Thr Pro Lys Thr Pro Thr Thr Pro Leu Pro Gln Thr Pro
 450 455 460

Thr Arg Arg Thr Glu Leu Tyr Ala Val Ile Asp Ile Glu Arg Thr Ala
 465 470 475 480

Ala Met Ser Asn Leu Gln Lys Ala Leu Pro Arg Asp Asp Gly Thr Ser
 485 490 495

Arg Lys Thr Arg His Asn Ser Thr Asp Leu Pro Met
 500 505

<210> 2

<211> 822

<212> PRT

<213> Mouse

<400> 2

Met Trp Gly Trp Lys Cys Leu Leu Phe Trp Ala Val Leu Val Thr Ala
 1 5 10 15

Thr Leu Cys Thr Ala Arg Pro Ala Pro Thr Leu Pro Glu Gln Ala Gln
 20 25 30

Pro Trp Gly Val Pro Val Glu Val Glu Ser Leu Leu Val His Pro Gly
 35 40 45

Asp Leu Leu Gln Leu Arg Cys Arg Leu Arg Asp Asp Val Gln Ser Ile
 50 55 60

Asn Trp Leu Arg Asp Gly Val Gln Leu Val Glu Ser Asn Arg Thr Arg
 65 70 75 80

Ile Thr Gly Glu Glu Val Glu Val Arg Asp Ser Ile Pro Ala Asp Ser
 85 90 95

Gly Leu Tyr Ala Cys Val Thr Ser Ser Pro Ser Gly Ser Asp Thr Thr
 100 105 110

Tyr Phe Ser Val Asn Val Ser Asp Ala Leu Pro Ser Ser Glu Asp Asp
 115 120 125

Asp Asp Asp Asp Asp Ser Ser Ser Glu Glu Lys Glu Thr Asp Asn Thr
 130 135 140

Lys Pro Asn Arg Arg Pro Val Ala Pro Tyr Trp Thr Ser Pro Glu Lys
 145 150 155 160

Met Glu Lys Lys Leu His Ala Val Pro Ala Ala Lys Thr Val Lys Phe
 165 170 175

Lys Cys Pro Ser Ser Gly Thr Pro Asn Pro Thr Leu Arg Trp Leu Lys
 180 185 190

Asn Gly Lys Glu Phe Lys Pro Asp His Arg Ile Gly Gly Tyr Lys Val
 195 200 205

Arg Tyr Ala Thr Trp Ser Ile Ile Met Asp Ser Val Val Pro Ser Asp
 210 215 220

Lys Gly Asn Tyr Thr Cys Ile Val Glu Asn Glu Tyr Gly Ser Ile Asn
 225 230 235 240

His Thr Tyr Gln Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile
 245 250 255

Leu Gln Ala Gly Leu Pro Ala Asn Glu Thr Val Ala Leu Gly Ser Asn
 260 265 270

Val Glu Phe Met Cys Lys Val Tyr Ser Asp Pro Gln Pro His Ile Gln
 275 280 285

Trp Leu Lys His Ile Glu Val Asn Gly Ser Lys Ile Gly Pro Asp Asn
 290 295 300

Leu Pro Tyr Val Gln Ile Leu Lys Thr Ala Gly Val Asn Thr Thr Asp
 305 310 315 320

Lys Glu Met Glu Val Leu His Leu Arg Asn Val Ser Phe Glu Asp Ala
 325 330 335

Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu Ser His His
 340 345 350

Ser Ala Trp Leu Thr Val Leu Glu Ala Leu Glu Glu Arg Pro Ala Val
 355 360 365
 Met Thr Ser Pro Leu Tyr Leu Glu Ile Ile Ile Tyr Cys Thr Gly Ala
 370 375 380
 Phe Leu Ile Ser Cys Met Leu Gly Ser Val Ile Ile Tyr Lys Met Lys
 385 390 395 400
 Ser Gly Thr Lys Lys Ser Asp Phe His Ser Gln Met Ala Val His Lys
 405 410 415
 Leu Ala Lys Ser Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Asp
 420 425 430
 Ser Ser Ala Ser Met Asn Ser Gly Val Leu Leu Val Arg Pro Ser Arg
 435 440 445
 Leu Ser Ser Ser Gly Thr Pro Met Pro Ala Gly Val Ser Glu Tyr Glu
 450 455 460
 Leu Pro Glu Asp Pro Arg Trp Glu Leu Pro Arg Asp Arg Leu Val Leu
 465 470 475 480
 Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Leu Ala Glu
 485 490 495
 Ala Ile Gly Leu Asp Lys Asp Lys Pro Asn Arg Val Thr Lys Val Ala
 500 505 510
 Val Lys Met Leu Lys Ser Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu
 515 520 525
 Ile Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile
 530 535 540
 Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile
 545 550 555 560
 Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Gln Ala Arg
 565 570 575
 Arg Pro Pro Gly Leu Glu Tyr Cys Tyr Asn Pro Ser His Asn Pro Glu
 580 585 590
 Glu Gln Leu Ser Ser Lys Asp Leu Val Ser Cys Ala Tyr Gln Val Ala
 595 600 605

Arg Gly Met Glu Tyr Leu Ala Ser Lys Lys Cys Ile His Arg Asp Leu
610 615 620

Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asn Val Met Lys Ile Ala
625 630 635 640

Asp Phe Gly Leu Ala Arg Asp Ile His His Ile Asp Tyr Tyr Lys Lys
645 650 655

Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu
660 665 670

Phe Asp Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val
675 680 685

Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Val
690 695 700

Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp
705 710 715 720

Lys Pro Ser Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys
725 730 735

Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu
740 745 750

Asp Leu Asp Arg Ile Val Ala Leu Thr Ser Ser Gln Glu Tyr Leu Asp
755 760 765

Leu Ser Ile Pro Leu Asp Gln Tyr Ser Pro Ser Phe Pro Asp Thr Arg
770 775 780

Ser Ser Thr Cys Ser Ser Gly Glu Asp Ser Val Phe Ser His Glu Pro
785 790 795 800

Leu Pro Glu Glu Pro Cys Leu Pro Arg His Pro Thr Gln Leu Ala Asn
805 810 815

Ser Gly Leu Lys Arg Arg
820

<210> 3

<211> 22

<212> PRT

<213> Mouse

<400> 3

His Ser Gln Met Ala Val His Lys Leu Ala Lys Ser Ile Pro Leu Arg

1

5

10

15

Arg Gln Val Thr Val Ser

20

<210> 4

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
tyrosine-phosphorylated peptide

<220>

<223> X = phosphotyrosine

<400> 4

Leu Val Ile Ala Gly Asn Pro Ala Xaa Arg Ser

1

5

10

<210> 5

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus

<220>

<223> Xaa can be any amino acid

<400> 5

Val Xaa Xaa Leu Xaa Xaa Xaa Ile Xaa Leu Xaa Arg Xaa Val Xaa Val

1

5

10

15

<210> 6

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: motif

<220>

<223> X in the 3rd position= any amino acid

<220>

<223> X in the 4th position= phosphotyrosine

<400> 6

Asn Pro Xaa Xaa

1

<210> 7

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
peptide derived from TrkA receptor

<400> 7

His Ile Ile Glu Asn Pro Gln Xaa Phe Ser Asp Ala

1

5

10